AMENDMENTS TO THE CLAIMS

1.-4. (Cancelled)

5. (Withdrawn) A computer-readable medium carrying a microsatellite polymorphic marker distribution map and one or more sequences of instructions from a user of a computer system for analyzing said markers over a desired human genomic region, wherein the distribution map comprises information regarding the position of microsatellite polymorphic markers over one or more regions of the human genome, said markers being positioned at intervals of from about 50 Kb to 150 Kb, wherein execution of one or more sequences of instructions by one or more processors causes the one or more processors to perform a method, comprising:

receiving a query inputted by the user and receiving instructions as to a microsatellite markers or a human genomic region to include in analysis;

accessing distribution map information stored on the medium;

displaying a map showing the position of markers on a human genomic region, wherein the map provides at least the selected markers or markers within the selected region.

6. (Withdrawn) The computer-readable medium of claim 5, wherein the medium additionally carries sequence information for the markers.

7. (Withdrawn) The computer-readable medium of claim 6, wherein the sequence information comprises nucleotide sequences of SEQ ID NOS: 1-27088.

8. (Withdrawn) An isolated polynucleotide useful as a primer, the polynucleotide being about 15 to 100 nucleotides in length and containing a nucleotide sequence extending in the 3'-direction from the 5'-terminus of a sequence of one of SEQ ID NOS: 1- 27088 or a nucleotide sequence complementary to a sequence extending in the 5'-direction from the 3'-terminus of a sequence of one of SEQ ID NOS: 1-27088.

9. (Withdrawn) A method of assessing susceptibility of a human subject to psoriasis vulgaris, the method comprising:

analyzing a region of about 111 kb extending from C1_2_6 to C2_4_4 for the presence of a marker that is associated with psoriasis vulgaris, wherein the marker is allele 303, allele 357, allele 255, allele 259, or allele 223;

wherein detection of the marker is indicative of susceptibility of the subject to psoriasis vulgaris.

10. (Withdrawn) The method of claim 9, wherein the marker is allele 303.

11. (Withdrawn) The method of claim 9, wherein the subject is heterozygous and is identified as a carrier for psoriasis vulgaris.

12. (Withdrawn) The method of claim 9, wherein the subject is homozygous, and is susceptible to onset or has psorasis vulgaris.

13. (**Currently Amended**) A method of identifying a DNA sequence fragment comprising a microsatellite in a human genomic region in which a gene associated with a phenotype exists, comprising:

selecting a combination of DNA sequences comprising SEQ ID Nos. 1-27088**,** wherein each of the sequences comprises a microsatellite genetic polymorphism marker;

collecting DNA samples from subjects affected with said phenotype and control subjects not affected with said phenotype;

performing polymerase chain reactions (PCR) on the DNA samples using forward primers consisting of 15-25 nucleotides wherein the forward primers consist of the same nucleotide sequence as the sequence extending in the 3'-direction from the 5'-terminus of each of the DNA sequences in said combination and reverse primers consisting of 15-25 nucleotides **wherein the reverse primers consist of the sequence complementary to the sequence** extending in the 5'-direction from the 3'-terminus of each of the DNA sequences in said combination to produce DNA sequence fragments, wherein each of said DNA sequence fragments comprises a microsatellite genetic polymorphism marker;

analyzing alleles of the microsatellite genetic polymorphism markers of said DNA sequence fragments; and

statistically comparing allele frequencies observed in the DNA sequence fragments produced from the affected subjects with those observed in the DNA sequence fragments produced from the control subjects to identify microsatellite polymorphism markers found positive whose allele frequencies observed in the DNA sequence fragments produced from the affected subjects are statistically significantly different from the allele frequencies observed in their corresponding DNA sequence fragments produced from the control subjects, wherein the DNA fragments comprising at least one microsatellite polymorphism marker found positive are in a human genomic region in which a gene associated with a phenotype exists.

14. (Previously Presented) The method according to claim 13, further comprising the step of mixing the DNA samples obtained from the subjects affected with the phenotype to provide pooled samples for affected subjects and mixing the DNA samples obtained from the control subjects not affected with the phenotype to provide pooled DNA samples for control subjects before performing the polymerase chain reaction.

15. (Previously Presented) The method according to claim 13, wherein the DNA sequence fragments produced by PCR comprise all or a part of the DNA sequences of SEQ ID Nos: 1-27088.

16. (Previously Presented) The method according to claim 13, wherein said analyzing of alleles of the microsatellite genetic polymorphism markers is carried out using a DNA chip and a mass spectrometer.

17. (**Currently Amended**) A method of identifying a DNA sequence fragment comprising a microsatellite in a human genomic region according to claim 13**,** further comprising:

selecting secondary DNA sequences containing at least one microsatellite polymorphism marker found positive through the method of claim 13 from the combination of DNA sequences comprising SEQ ID Nos. 1-27088;

collecting DNA samples from affected subjects different from the subjects affected with the phenotype of claim 13 and control subjects different from the control subjects of claim 13;

performing polymerase chain reaction (PCR) on the DNA samples using forward primers consisting of 15-25 nucleotides wherein the forward primers consist of the same nucleotide sequence as the sequence extending in the 3'-direction from the 5'-terminus of each of the secondary DNA sequences and reverse primers consisting of 15-25 nucleotides **wherein the reverse primers consist of the sequence complementary to the sequence** extending in the 5'-direction from the 3'-terminus of each of the secondary DNA sequences to produce secondary DNA sequence fragments;

analyzing alleles of the microsatellite genetic polymorphism markers of said secondary DNA sequence fragments, and

statistically comparing allele frequencies observed in the secondary DNA sequence fragments produced from the affected subjects with those observed in the secondary DNA sequence fragments produced from the control subjects to identify microsatellite polymorphism markers found true-positive whose allele frequencies observed in the secondary DNA sequence fragments produced from the affected subjects are statistically significantly different from allele frequencies observed in their corresponding secondary DNA sequence fragments produced from the control subjects, wherein the secondary DNA fragments comprising at least one microsatellite polymorphism marker found true-positive are regarded as a region in which a pathogenic gene or a gene relating to human phenotypes associated with a genetic factor exists with higher probability.

18. (Cancelled)

19. (Previously Presented) The method according to claim 13, further comprising:

analyzing said DNA sequence fragments comprising at least one microsatellite polymorphism marker found positive through the method of claim 13, based on allele frequency of known single nucleotide polymorphisms.

20. (Previously Presented) The method according to claim 17, further comprising:

analyzing said DNA sequence fragments comprising at least one microsatellite polymorphism marker found true-positive through the method of claim 17, based on allele frequency of known single nucleotide polymorphisms.